

EXHIBIT 6



AGC GGC TGG GAG GGC CGC TTC TGC CAG CGC GGTGAGGGGG AGAGGTGGAT Ser Gly Trp Glu Gly Arg Phe Cys Gln Arg 91	3236
GCTGGCGGGC GGCGGGGCGG GGCTGGGGCC GGGTTGGGGG CGCGGCACCA GCACCAGCTG CCCGCGCCCT CCCCTGCCCC CA GAG GTG AGC TTC CTC AAT TGC TCT CTG GAC Glu Val Ser Phe Leu Asn Cys Ser Leu Asp 92	3296 3348
AAC GGC GGC TGC ACG CAT TAC TGC CTA GAG GAG GTG GGC TGG CGG CGC Asn Gly Gly Cys Thr His Tyr Cys Leu Glu Glu Val Gly Trp Arg Arg	3396
TGT AGC TGT GCG CCT GGC TAC AAG CTG GGG GAC GAC CTC CTG CAG TGT Cys Ser Cys Ala Pro Gly Tyr Lys Leu Gly Asp Asp Leu Leu Gln Cys	3444
CAC CCC GCA GGTGAGAAGC CCCCAATACA TCGCCAGGA ATCACGCTGG His Pro Ala 136	3493
GTGCGGGGTG GGCAGGCCCC TGACGGGCGC GGC CGGGGG GCTCAGGAGG GTTCTAGGG	3553
AGGGAGCGAG GAACAGAGTT GAGCCTTGGG GCAGCGGCAG ACGCGCCCAA CACCGGGGCC	3613
ACTGTTAGCG CAATCAGCCC GGGAGCTGGG CGCGCCCTCC GCTTCCCTG CTTCCTTTCT	3673
TCCTGGCGTC CCCGCTTCT CCGGGCGCCC CTGCGACCTG GGGCCACCTC CTGGAGCGCA	3733
AGCCCAAGTGG TGGCTCCGCT CCCAGTCTG AGCGTATCTG GGGCGAGGCG TGCAGCGTCC	3793
TCCTCCATGT AGCCTGGCTG CGTTTTTCTC TGACGTTGTC CGGCGTGCAT CGCATTTCCC	3853
TCTTTACCCC CTTGCTTCT TGAGGAGAGA ACAGAATCCC GATTCTGCCT TCTTCTATAT	3913
TTTCCTTTTT ATGCATTTTA ATCAAATTTA TATATGTATG AAACTTTAAA AATCAGAGTT	3973
TTACAACTCT TACACTTTCA GCATGCTGTT CCTTGGCATG GGTCTTTTT TCATTCAATT	4033
TCATAAAAGG TGGACCCCTT TAATGTGGAA ATTCCTATCT TCTGCCTCTA GGGCATTAT	4093
CATTATTTT TTCTACAATC TCCCCTTTAC TTCCTCTATT TTCTCTTTCT GGACCTCCCA	4153
TTATTAGAC CTCTTTCCTC TAGTTTTATT GTCTCTTCTA TTTCCCATCT CTTTGACTTT	4213
GTGTTTTCTT TCAGGGAACT TTCTTTTTTT TCTTTTTTTT TGAGATGGAG TTCACTCTT	4273
GTTGTCCCAG GCTGGAGTGC AATGACGTGA TCTCAGCTCA CCACAACCTC CGCTCCTGG	4333
ATTCAAGCGA TTCTCCTGCC GCAGCCTCCC GAGTAGCTGG GATTACAGGC ATGCGCCACC	4393
ACGCCCAGCT AATTTTGTGT TTTTAGTAGA GAAGGGGTTT CTCCGTGTTG GTCAAGCTGG	4453

FIG. 2D

CTG GCC TGC GGG GCA GTG CTC ATC CAC CCC TCC TGG GTG CTG ACA GCG 7213
Leu Ala Cys Gly Ala Val Leu Ile His Pro Ser Trp Val Leu Thr Ala

GCC CAC TGC ATG GAT GAG TCC AAG AAG CTC CTT GTC AGG CTT 7255
Ala His Cys Met Asp Glu Ser Lys Lys Leu Leu Val Arg Leu
223

GGTATGGGCT GGAGCCAGGC AGAAGGGGGC TGCCAGAGGC CTGGGTAGGG GGACCAGGCA 7315

GGCTGTTGAG GTTTGGGGGA CCCCCTCC CAGGTGCTTA AGCAAGAGGC TTCTTGAGCT 7375

CCACAGAAGG TGTTTGGGGG GAAGAGGCCT ATGTGCCCCC ACCCTGCCCC CCCATGTACA 7435

CCCAGTATTT TGCAGTAGGG GGTCTCTGG TGCCCTCTTC GAATCTGGGC ACAGGTACCT 7495

GCACACACAT GTTTGTGAGG GGCTACACAG ACCTTCACCT CTCCACTCCC ACTCATGAGG 7555

AGCAGGCTGT GTGGGCCTCA GCACCCCTGG GTGCAGAGAC CAGCAAGGCC TGGCCTCAGG 7615

GCTGTGCCTC CCACAGACTG ACAGGGATGG AGCTGTACAG AGGGAGCCCT AGCATCTGCC 7675

AAAGCCACAA GCTGCTTCCC TAGCAGGCTG GGGGCTCCTA TGCATTGGCC CCGATCTATG 7735

GCAATTTCTG GAGGGGGGGT CTGGCTCAAC TCTTTCTGCC AAAAGAAGG CAAAGCATAT 7795

TGAGAAAGGC CAAATTCACA TTTCTACAG CATAATCTAT GCCAGTGCC CCGTGGGGCT 7855

TGGCTTAGAA TTCCAGGTG CTCTTCCCAG GGAACCATCA GTCTGGACTG AGAGGACCTT 7915

CTCTCTCAGG TGGGACCCGG CCCTGTCTC CCTGGCAGTG CCGTGTCTG GGGGTCTCC 7975

TCTCTGGGTC TACTGCCCC TGGGGTCTCT CCAGCTACCT TTGCTCCATG TTCCTTTGTG 8035

GCTCTGGTCT GTGTCTGGGG TTTCCAGGGG TCTCGGGCTT CCCTGCTGCC CATTCTTCT 8095

CTGGTCTCAC GGCTCCGTGA CTCCTGAAAA CCAACCAGCA TCCTACCCCT TTGGATTGAC 8155

ACCTGTTGGC CACTCCTTCT GGCAGGAAAA GTCACCGTTG ATAGGGTTCC ACGGCATAGA 8215

CAGGTGGCTC CGCGCCAGTG CCTGGGACGT GTGGGTGCAC AGTCTCCGGG TGAACCTTCT 8275

TCAGGCCCTC TCCCAGGCCT GCAGGGGCAC ACCAGTGGGT GGGCCTCAGG AAAGTGCCAC 8335

TGGGGAGAGG CTCCCCGCAG CCCACTCTGA CTGTGCCCTC TGCCCTGCA GGA GAG 8390
Gly Glu
224

TAT GAC CTG CGG CGC TGG GAG AAG TGG GAG CTG GAC CTG GAC ATC AAG 8438
Tyr Asp Leu Arg Arg Trp Glu Lys Trp Glu Leu Asp Leu Asp Ile Lys

FIG. 2G

CGG CGA ACT																-42
TGG	AGT	ATC	TCC	ACG	ACC	CCC	CCC	TGT	GCC	AGT	CCC	TCC	AGA	ATG	TGG	6
														Met	Trp	
														-42		
CAG	CTC	ACA	AGC	CTC	CTG	CTG	TTC	GTG	GCC	ACC	TGG	GGA	ATT	TCC	GGC	54
Gln	Leu	Thr	Ser	Leu	Leu	Leu	Phe	Val	Ala	Thr	Trp	Gly	Ile	Ser	Gly	
										-30						
ACA	CCA	GCT	CCT	CTT	GAC	TCA	GTG	TTC	TCC	AGC	AGC	GAG	CGT	GCC	CAC	102
Thr	Pro	Ala	Pro	Leu	Asp	Ser	Val	Phe	Ser	Ser	Ser	Glu	Arg	Ala	His	
														-20		
														-10		
CAG	GTG	CTG	CGG	ATC	CGC	AAA	CGT	GCC	AAC	TCC	TTC	CTG	GAG	GAG	CTC	150
Gln	Val	Leu	Arg	Ile	Arg	Lys	Arg	Ala	Asn	Ser	Phe	Leu	Glu	Glu	Leu	
										-1	+1					
CGT	CAC	AGC	AGC	CTG	GAG	CGG	GAG	TGC	ATA	GAG	GAG	ATC	TGT	GAC	TTC	198
Arg	His	Ser	Ser	Leu	Glu	Arg	Glu	Cys	Ile	Glu	Glu	Ile	Cys	Asp	Phe	
												10				
												20				
GAG	GAG	GCC	AAG	GAA	ATT	TTC	CAA	AAT	GTG	GAT	GAC	ACA	CTG	GCC	TTC	246
Glu	Glu	Ala	Lys	Glu	Ile	Phe	Gln	Asn	Val	Asp	Asp	Thr	Leu	Ala	Phe	
														30		
														40		
TGG	TCC	AAG	CAC	GTC	GAC	GGT	GAC	CAG	TGC	TTG	GTC	TTG	CCC	TTG	GAG	294
Trp	Ser	Lys	His	Val	Asp	Gly	Asp	Gln	Cys	Leu	Val	Leu	Pro	Leu	Glu	
										50						
CAC	CCG	TGC	GCC	AGC	CTG	TGC	TGC	GGG	CAC	GGC	ACG	TGC	ATC	GAC	GGC	342
His	Pro	Cys	Ala	Ser	Leu	Cys	Cys	Gly	His	Gly	Thr	Cys	Ile	Asp	Gly	
													60			
													70			
ATC	GGC	AGC	TTC	AGC	TGC	GAC	TGC	CGC	AGC	GGC	TGG	GAG	GGC	CGC	TTC	390
Ile	Gly	Ser	Phe	Ser	Cys	Asp	Cys	Arg	Ser	Gly	Trp	Glu	Gly	Arg	Phe	
										80						
TGC	CAG	CGC	GAG	GTG	AGC	TTC	CTC	AAT	TGC	TCT	CTG	GAC	AAC	GGC	GGC	438
Cys	Gln	Arg	Glu	Val	Ser	Phe	Leu	Asn	Cys	Ser	Leu	Asp	Asn	Gly	Gly	
										90						
										100						
TGC	ACG	CAT	TAC	TGC	CTA	GAG	GAG	GTG	GGC	TGG	CGG	CGC	TGT	AGC	TGT	486
Cys	Thr	His	Tyr	Cys	Leu	Glu	Glu	Val	Gly	Trp	Arg	Arg	Cys	Ser	Cys	
														110		
														120		
GCG	CCT	GGC	TAC	AAG	CTG	GGG	GAC	GAC	CTC	CTG	CAG	TGT	CAC	CCC	GCA	534
Ala	Pro	Gly	Tyr	Lys	Leu	Gly	Asp	Asp	Leu	Leu	Gln	Cys	His	Pro	Ala	
										130						
GTG	AAG	TTC	CCT	TGT	GGG	AGG	CCC	TGG	AAG	CGG	ATG	GAG	AAG	AAG	CGC	582
Val	Lys	Phe	Pro	Cys	Gly	Arg	Pro	Trp	Lys	Arg	Met	Glu	Lys	Lys	Arg	
														140		
														150		

FIG. 3A

AGT CAC CTG AAA CGA GAC ACA GAA GAC CAA GAA GAC CAA GTA GAT CCG 630
Ser His Leu Lys Arg Asp Thr Glu Asp Gln Glu Asp Gln Val Asp Pro
160

CGG CTC ATT GAT GGG AAG ATG ACC AGG CGG GGA GAC AGC CCC TGG CAG 678
Arg Leu Ile Asp Gly Lys Met Thr Arg Arg Gly Asp Ser Pro Trp Gln
170 180

GTG GTC CTG CTG GAC TCA AAG AAG AAG CTG GCC TGC GGG GCA GTG CTC 726
Val Val Leu Leu Asp Ser Lys Lys Lys Leu Ala Cys Gly Ala Val Leu
190 200

ATC CAC CCC TCC TGG GTG CTG ACA GCG GCC CAC TGC ATG GAC GAG TCC 774
Ile His Pro Ser Trp Val Leu Thr Ala Ala His Cys Met Asp Glu Ser
210

AAG AAG CTC CTT GTC AGG CTT GGA GAG TAT GAC CTG CGG CGC TGG GAG 822
Lys Lys Leu Leu Val Arg Leu Gly Glu Tyr Asp Leu Arg Arg Trp Glu
220 230

AAG TGG GAG CTG GAC CTG GAC ATC AAG GAG GTC TTC GTC CAC CCC AAC 870
Lys Trp Glu Leu Asp Leu Asp Ile Lys Glu Val Phe Val His Pro Asn
240

TAC AGC AAG AGC ACC ACC GAC AAT GAC ATC GCA CTG CTG CAC CTG GCC 918
Tyr Ser Lys Ser Thr Thr Asp Asn Asp Ile Ala Leu Leu His Leu Ala
250 260

CAG CCC GCC ACC CTC TCG CAG ACC ATA GTG CCC ATC TGC CTC CCG GAC 966
Gln Pro Ala Thr Leu Ser Gln Thr Ile Val Pro Ile Cys Leu Pro Asp
270 280

AGC GGC CTT GCA GAG CGC GAG CTC AAT CAG GCC GGC CAG GAG ACC CTC 1014
Ser Gly Leu Ala Glu Arg Glu Leu Asn Gln Ala Gly Gln Glu Thr Leu
290

GTG ACG GGC TGG GGC TAC CAC AGC AGC CGA GAG AAG GAG GCC AAG AGA 1062
Val Thr Gly Trp Gly Tyr His Ser Ser Arg Glu Lys Glu Ala Lys Arg
300 310

AAC CGC ACC TTC GTC CTC AAC TTC ATC AAG ATT CCC GTG GTC CCG CAC 1110
Asn Arg Thr Phe Val Leu Asn Phe Ile Lys Ile Pro Val Val Pro His
320

AAT GAG TGC AGC GAG GTC ATG AGC AAC ATG GTG TCT GAG AAC ATG CTG 1158
Asn Glu Cys Ser Glu Val Met Ser Asn Met Val Ser Glu Asn Met Leu
330 340

TGT GCG GGC ATC CTC GGG GAC CGG CAG GAT GCC TGC GAG GGC GAC AGT 1206
Cys Ala Gly Ile Leu Gly Asp Arg Gln Asp Ala Cys Glu Gly Asp Ser
350 360

GGG GGG CCC ATG GTC GCC TCC TTC CAC GGC ACC TGG TTC CTG GTG GGC 1254
Gly Gly Pro Met Val Ala Ser Phe His Gly Thr Trp Phe Leu Val Gly
370

FIG. 3B